In re Application of: Doron LANCET et al
Serial No.: 10/511,278
Filed: October 22, 2004
Office Action Mailing Date: March 27, 2007

Examiner: Carla J. MYERS
Group Art Unit: 1634
Attorney Docket: 28364

IN THE SPECIFICATION

On pages 7 (lines 10-16), replace the existing paragraph with:

FIG. 1 illustrates the olfactory receptor (OR) gene cluster on human chromosome 17p13.3. Genes are positioned in their correct order and orientation, with exons marked as triangles and introns marked as squares. The regions that were sequenced are filled. The serial numbers of individual SNPs analyzed within each OR gene are shown inside ovals and are corresponding to the list detailed elsewhere (http://bioinfoDOTweizmannDOTacDOTil/~menashe/OR17_SNPs.html)~~(http://bioinfo.weizmann.ac.il/~menashe/OR17_SNPs.html)~~. The span of the three intervals used for Clark's algorithm is indicated with Roman numerals I-III.

Page 11 (lines 16-21) , replace the existing paragraph with:

LD and recombination - The coefficient *D'* (Lewontin, 1964) was used as a measure of LD between polymorphic sites, using the Graphical Overview of Linkage Disequilibrium (GOLD) software (Abecasis and Cookson, 2000), applying a Fisher exact test (FET) for statistical significance. An alternative method used for pairwise LD computation was the Expectation Maximization (EM) algorithm (Excoffier, 1995) using the Arlequin software (http://lgbDOTunigeDOTch/arlequin) ~~(http://lgb.unige.ch/arlequin)~~.

Page 12 (lines 3 to 8), replace the existing paragraph with:

A total of 74 polymorphic sites were found, of which 31 were novel (http://bioinfoDOTweizmannDOTacDOTil/~menashe/OR17_SNPs.html) ~~(http://bioinfo.weizmann.ac.il/~menashe/OR17_SNPs.html)~~. Two of the SNPs identified, in pseudogenes OR1P1P and OR1E3P segregated between the pseudogenized and intact forms. Noteworthy, the variability within the same two ORs displayed significant deviations from Hardy-Weinberg equilibrium, whereby 7 out of 10 SNPs (singletons excluded) were not at equilibrium (Table 2).

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Page 14 (lines 1-2), replace the existing text with:

(http://bioinfoDOTweizmannDOTacDOTil/~menashe/OR17_SNPs.html) ~~(http://bioinfo.weizmann.ac.il/~menashe/OR17_SNPs.html)~~ these results probably do not reflect non-specific PCR amplifications of two highly similar ORs.

Page 50 (lines 23 to 33), replace the existing paragraph with:

Computation of the number of OR SPGs in the entire genome - The number of OR SPGs in the entire human genome was computed for 189 individuals by a two-step procedure. In the first step, based on the discovery of 11 OR SPGs among 50 singly disrupted pseudogenes tested, it was estimated that for the total of 67 such genes in the HORDE database (http://bioinformaticsDOTweizmannDOTacDOTil/HORDE/index.html) ~~(http://bioinformatics.weizmann.ac.il/HORDE/)~~ there would be a proportionate number of 15 SPGs genome-wide. The assumption was that OR pseudogenes with more than one disrupting mutation are unlikely to harbor SPGs. In the second step, based on a sequencing depth of five chromosomes in the Celera SNP database (Venter et al., 2001), and assuming a neutral frequency spectrum for the disrupted derived alleles, the SPG count of 15 in 5 chromosomes extrapolates to 45 SPGs in 378 chromosomes (189 individuals). Thus, a total of 60 SPGs was computed